



Sequences producing significant alignments:		Score	E
		(bits)	Value
gi 13899257 ref NP_113622.1	chromosome 7 open reading fram...	728	0.0
gi 11967945 ref NP_071863.1	hypothetical protein, clone 1-...	633	e-180
gi 38454298 ref NP_942076.1	Unknown (protein for MGC:72996...)	515	e-144
gi 40807187 gb AAH65312.1	Unknown (protein for MGC:77146) ...	225	3e-57
gi 38091832 ref XP_126502.2	RIKEN cDNA 2010008E23 [Mus mus...	158	4e-37
gi 16740606 gb AAH16187.1	RIKEN cDNA 2010008E23 gene [Mus ...	158	4e-37
gi 20988715 gb AAH29841.1	2010008E23Rik protein [Mus muscu...	158	4e-37
gi 12842172 dbj BAB25500.1	unnamed protein product [Mus mu...	151	3e-35
gi 28973799 ref NP_803190.1	hypothetical protein MGC3123 [...]	151	4e-35
gi 33341676 gb AAQ15209.1	FP2653 [Homo sapiens] >gi 371826...	151	4e-35
gi 27689889 ref XP_221010.1	similar to RIKEN cDNA 2010008E...	144	5e-33
gi 22204247 emb CAD43429.1	SI:dz180G5.5 (novel ubiquitin) ...	108	2e-22
gi 10433006 dbj BAB13886.1	unnamed protein product [Homo s...	68	4e-10
gi 283528 pir IS27786	acidic protein - Caenorhabditis elega...	55	3e-06
gi 17551804 ref NP_498916.1	ubiquitin domain containing pr...	55	3e-06
gi 39585075 emb CAE62726.1	Hypothetical protein CBG06886 [...]	54	7e-06
gi 13129118 ref NP_077012.1	hypothetical protein MGC3123 [...]	47	0.001
gi 41616494 tpg DAA03341.1	TPA: HDC18999 [Drosophila melan...	45	0.005
gi 30348407 emb CAC84278.1	stpc [Saimiriine herpesvirus 2]...	44	0.008
gi 38174711 gb AAH61325.1	MGC75814 protein [Xenopus tropic...	43	0.015

gi 17384405 emb CAD13245.1	bA113O24.1 (similar to insulin-...)	43	0.015
gi 30348416 emb CAC84992.1	saimiri transformation-associat...	43	0.020
gi 41616370 tpq DAA03279.1	TPA: HDC18148 [Drosophila melan...	43	0.020
gi 1743279 emb CAA67869.1	StpC139 [Saimiriine herpesvirus 2]	43	0.020
gi 41617660 tpq DAA02769.1	TPA: HDC08319 [Drosophila melan...	42	0.027
gi 9256600 ref NP_061722.1	protocadherin alpha subfamily C...	42	0.027
gi 14165431 ref NP_114089.1	protocadherin alpha subfamily ...	42	0.027
gi 43107036 gb EAC19557.1	unknown [environmental sequence]	42	0.027
gi 41327160 ref NP_898828.1	trinucleotide repeat containin...	42	0.027
gi 16933557 ref NP_003728.1	protocadherin 16 precursor; fi...	42	0.027
gi 2565063 gb AAB91442.1	CTG4a [Homo sapiens]	42	0.027
gi 38648766 gb AAH63288.1	PCDHAC2 protein [Homo sapiens]	42	0.027
gi 43693587 gb EAF02012.1	unknown [environmental sequence]	42	0.027
gi 33942072 ref NP_006577.2	trinucleotide repeat containin...	42	0.027
gi 43203317 gb EAC67209.1	unknown [environmental sequence]	42	0.036
gi 30354634 gb AAH51836.1	LRP8 protein [Homo sapiens]	42	0.036
gi 34865759 ref XP_243524.2	similar to lipoprotein recepto...	41	0.049
gi 15825005 gb AAL09566.1	lipoprotein receptor-related pro...	41	0.049
gi 6678720 ref NP_032538.1	low density lipoprotein recepto...	41	0.049
gi 300162 gb AAB26494.1	alpha-2-macroglobulin receptor, A2...	41	0.049
gi 26349007 dbj BAC38143.1	unnamed protein product [Mus mu...	41	0.049
gi 27881830 gb AAH43675.1	Lrp1 protein [Mus musculus]	41	0.049
gi 15825096 gb AAL09567.1	lipoprotein receptor-related pro...	41	0.049
gi 15529624 gb AAL01375.1	PTPRE [Homo sapiens]	41	0.066
gi 5729993 ref NP_006495.1	protein tyrosine phosphatase, r...	41	0.066
gi 32405458 ref XP_323342.1	predicted protein [Neurospora ...	41	0.066
gi 116896 sp P22576 COLL_SHV2C	Collagen-like protein >gi 93...	41	0.088
gi 30348404 emb CAC84986.1	saimiri transformation-associat...	41	0.088
gi 21166382 ref NP_620063.1	neurexin 2 isoform beta precur...	41	0.088
gi 1743282 emb CAA67871.1	StpC484 [Saimiriine herpesvirus 2]	41	0.088
gi 4758686 ref NP_002323.1	low density lipoprotein-related...	40	0.12
gi 28379108 ref NP_786000.1	integral membrane protein [Lac...	40	0.12
gi 17028418 gb AAH17526.1	Tnfrsf25 protein [Mus musculus]	40	0.16
gi 14279974 gb AAK58831.1	lyosphosphatidic acid acyltransf...	40	0.16
gi 17975768 ref NP_004434.2	ephrin receptor EphB3 precurso...	40	0.16
gi 41617130 tpq DAA02504.1	TPA: HDC06391 [Drosophila melan...	40	0.16
gi 14279976 gb AAK58832.1	lysophosphatidic acid acyltransf...	40	0.16
gi 32407261 ref XP_324215.1	predicted protein [Neurospora ...	40	0.16
gi 4758688 ref NP_004622.1	low density lipoprotein recepto...	40	0.16
gi 1708164 sp P54753 EPB3_HUMAN	Ephrin type-B receptor 3 pr...	40	0.16
gi 15451868 ref NP_150643.1	low density lipoprotein recept...	40	0.16
gi 15451866 ref NP_059992.2	low density lipoprotein recept...	40	0.16
gi 41386737 ref NP_803484.1	1-acylglycerol-3-phosphate O-a...	40	0.16
gi 1834534 emb CAA9509.1	apolipoprotein E receptor 2 906 ...	40	0.16
gi 43873036 gb EAF90508.1	unknown [environmental sequence]	39	0.21
gi 23463263 ref NP_695206.1	prepro-Neuropeptide W polypept...	39	0.21
gi 44580550 gb EAK25059.1	unknown [environmental sequence]	39	0.21
gi 38512117 gb AAH61796.1	Adam15 protein [Rattus norvegicus]	39	0.21
gi 34877564 ref XP_214295.2	similar to hypothetical protei...	39	0.21
gi 41617360 tpq DAA02619.1	TPA: HDC07244 [Drosophila melan...	39	0.21

gi 9945328 ref NP_064704.1	a disintegrin and metalloprotei...	39	0.21	
gi 33355652 gb AAQ16195.1	latent membrane protein 1 [Human...]	39	0.21	
gi 43032543 gb EAB82911.1	unknown [environmental sequence]	39	0.21	
gi 43287536 gb EAD09607.1	unknown [environmental sequence]	39	0.21	
gi 43732193 gb EAF20862.1	unknown [environmental sequence]	39	0.21	
gi 13236579 ref NP_077306.1	solute carrier family 27 membe...	39	0.29	
gi 24642080 ref NP_727818.1	CG32594-PD [Drosophila melanog...	39	0.29	
gi 5441942 gb AAD43187.1	supported by mouse EST AA538043 (...)	39	0.29	
gi 28870062 ref NP_792681.1	conserved hypothetical protein...	39	0.29	
gi 16763443 ref NP_459058.1	putative transcriptional regul...	39	0.29	
gi 14042219 dbj BAB55156.1	unnamed protein product [Homo s...	39	0.29	
gi 346951 pir A44399	stromelysin 3 (EC 3.4.24.-) - mouse	39	0.29	
gi 23471875 ref ZP_00127203.1	COG2304: Uncharacterized pro...	39	0.29	
gi 18676616 dbj BAB84960.1	FLJ00207 protein [Homo sapiens]	39	0.29	
gi 42662491 ref XP_117224.5	similar to RIKEN cDNA 0610009J...	39	0.29	
gi 13385766 ref NP_080533.1	socius [Mus musculus] >gi 1285...	39	0.29	
gi 7715870 gb AAF68173.1	mannose 6-phosphate/insulin-like ...	39	0.29	
gi 34331084 dbj BAC86050.1	unnamed protein product [Homo s...	39	0.29	
gi 26339360 dbj BAC33351.1	unnamed protein product [Mus mu...	39	0.29	
gi 34852277 ref XP_215351.2	similar to cysteine-rich prote...	39	0.29	
gi 23104640 ref ZP_00091102.1	hypothetical protein [Azotob...	38	0.51	
gi 6678894 ref NP_032632.1	matrix metalloproteinase 11; st...	38	0.51	
gi 31543531 ref NP_035342.2	protein tyrosine phosphatase, ...	38	0.51	
gi 2507226 sp P49446 PTPE_MOUSE	Protein-tyrosine phosphatases...	38	0.51	
gi 33355648 gb AAQ16193.1	latent membrane protein 1 [Human...]	38	0.51	
gi 41619762 tpg DAA04313.1	TPA: HDC15396 [Drosophila melan...	38	0.51	
gi 7439344 pir JCE132	protein-tyrosine-phosphatase (EC 3.1...	38	0.51	
gi 4406172 gb AAD19887.1	latent membrane protein-1 [Human ...]	38	0.51	
gi 7435843 pir JCE197	stromelysin 3 (EC 3.4.24.-) - rat	38	0.51	
gi 38374134 gb AAR19270.1	latent membrane protein 1 [Human...]	38	0.51	

Alignments

Get selected sequences Select all Deselect all

[] >gi|13899257|ref|NP_113622.1| chromosome 7 open reading frame 21 [Homo sapiens]
 gi|34922062|sp|Q98VT8|CG21_HUMAN Protein C7orf21 (SB144)
 gi|12654233|gb|AAH00936.1| C7orf21 protein [Homo sapiens]
 gi|21303411|gb|AAK67645.1| hypothetical membrane protein SB144 precursor [Homo s
 gi|21620058|gb|AAR33182.1| Chromosome 7 open reading frame 21 [Homo sapiens]
 gi|37182085|gb|AAQ88845.1| TLIE763 [Homo sapiens]
 Length = 246

Score = 728 bits (1709), Expect = 0.0

Identities = 236/245 (96%), Positives = 236/245 (96%), Gaps = 5/245 (2%)

Query: 1 TLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEKGDPPLQPQSGTPTPSQPSMM--TDS 58

TLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEKGDPPLQPQSGTPTPSQPS M TDS

Sbjct: 2 TLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEKGDPPLQPQSGTPTPSQPSAAMAATDS 61

Query: 59 MRGEAPGAETPSLRHRGQM-QPEPSTGFTATPPAPDSPQEPLVRLKFLNDSEQVAM-WP 116

MRGEAPGAETPSLRHRGQ QPEPSTGFTATPPAPDSPQEPLVLRLKFLNDSEQVA WP
 Sbjct: 62 MRGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRLKFLNDSEQVARAWP 121

Query: 117 HDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPNPP 176
 HDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSIHLPPNCVLHCHVSTRVGPNPP
 Sbjct: 122 HDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPNPP 181

Query: 177 CPPGSEPGPSGLEIGSLLLPI, LLLLLLWYCQI QYRPFFPLTATLGLAGFTLLSLLAF 236
 CPPGSEPGPSGLEIGSLLLPI, LLLLLWYCQI QYRPFFPLTATLGLAGFTLLSLLAF
 Sbjct: 182 CPPGSEPGPSGLEIGSLLLPLL, LLLLLLWYCQI QYRPFFPLTATLGLAGFTLLSLLAF 241

Query: 237 -MYRP 240
 MYRP
 Sbjct: 242 AMYRP 246

[gi|11967945|ref|NP_071863.1] hypothetical protein, clone 1-2 [Mus musculus]
 gi|34922148|sp|Q9JMG3|CG21_MOUSE Protein C7orf21 homolog
 gi|7259236|dbj|BA92747.1| contains transmembrane (TM) region [Mus musculus]
 gi|12842088|dbj|BAB25465.1| unnamed protein product [Mus musculus]
 gi|18043424|gb|AAH19547.1| Hypothetical protein, clone 1-2 [Mus musculus]
 Length = 245

Score = 633 bits (1487), Expect = e-180
 Identities = 213/244 (87%), Positives = 222/244 (90%), Gaps = 6/244 (2%)

Query: 2 LIEVGVDVTVLFSVLACLLVIALAWVSTHTAEGGDPLPQPSGTPTPSQPS--MMMTDSM 59
 LIEVGVDVTVLF+VLACLLVLALAWVSTHT E DP PQP GT TP+QPS M +DS+
 Sbjct: 3 LIEVGVDVTVLFAVLACLLVLALAWVSTHTTESTDPQFQPPGTTPAQPSEAMSASDSI 62

Query: 60 RGEAPGAETPSLRHRGQM-QPEPSTGFTATPPAPDSPQEPLVLRLKFLNDSEQVAM-WPH 117
 R EAPGAE+PSLRHRG QPEP TG TA+ P PDSPQEPL+LRLKFLNDSEQVA WP
 Sbjct: 63 REEAPGAESPSLRHRGPSAQPEPDTGVTASTP-PDSPQEPLLRLKFLNDSEQVARAWPQ 121

Query: 118 DTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPNPPC 177
 DTIGSLKRTQFPG+EQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPP+PPC
 Sbjct: 122 DTIGSLKRTQFPGQEQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPHPPC 181

Query: 178 PPGSEPGPSGLEIGS, LLLPL, LLLWYCQI QYRPFFPLTATLGLAGFTL, LSLLAF- 236
 PPGSEPGPSGLEIGSLLLPLL, LLLWYCQI QYRPFFPLTATLGLAGFTLLSLLAF
 Sbjct: 182 PPGSEPGPSGLEIGSLLLPLL, LLLWYCQI QYRPFFPLTATLGLAGFTLLSLLAFA 241

Query: 237 MYRP 240
 MYRP
 Sbjct: 242 MYRP 245

[gi|38454298|ref|NP_942076.1| Unknown (protein for MGC:72996) [Rattus norvegicus]
 gi|37589846|gb|AAH59162.1| Unknown (protein for MGC:72996) [Rattus norvegicus]
 Length = 190

Score = 515 bits (1207), Expect = e-144
 Identities = 171/191 (89%), Positives = 176/191 (92%), Gaps = 6/191 (3%)

Query: 55 MT--DSMRGEAPGAETPSLRHRGQM-QPEPSTGFTATPPAPDSPQEPLVLRLKFLNDSEQ 111
 MT DS+R EAPGAE+PSLRHRG QPEP G TA+ P PDSPQEPL+LRLKFLNDSEQ

Sbjct: 1 MTAIDSIREEAPGAESPSLRHRGSAQPEPEAGVTASTP-PDSPQEPLLLRLKFLNDSEQ 59
 Query: 112 VAM-WPHDTIGSLKRTQFPGRQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRV 170
 VA WP DTIGSLKRTQFPGRQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRV
 Sbjct: 60 VARAWPQDTIGSLKRTQFPGRQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRV 119
 Query: 171 GPPNPPCPGSEPGPSGLEIGSLLLPLLLLLLWYCQIQYRPFFPLTATLGLAGFTLL 230
 GPP+PPCPGSEPGPSGLEIGSLLLPLLLLLLWYCQIQYRPFFPLTATLGLAGFTLL
 Sbjct: 120 GPPHPPCPGSEPGPSGLEIGSLLLPLLLLLLWYCQIQYRPFFPLTATLGLAGFTLL 179
 Query: 231 LSLLAF-MYRP 240
 LSLLAF MYRP
 Sbjct: 180 LSLLAFAMYRP 190

[>gi|40807187|gb|AAH65312.1] Unknown (protein for MGC:77146) [Danio rerio]
 Length = 292
 Score = 225 bits (523), Expect = 3e-57
 Identities = 136/319 (42%), Positives = 163/319 (51%), Gaps = 111/319 (34%)
 Query: 2 LIEGVGDEVTVLFSV--LACLVLALAWVSTHTAEGGDPL--PQPSGTP---TPSQ-PSM 53
 LIEGVGDEVT+LF V L LVL LAW STHT E + L P P +P T SQ P
 Sbjct: 3 LIEVGDEVTLLFGVVFLV--LVLVLAWASTHTVEPPEHLLSPSPGASPSTETDSQEP-- 58
 Query: 54 MM----TDS---MRGE---APGAETPS-----LRHR 74
 + TDS +R E PG E + LRHR
 Sbjct: 59 -LPPGNTDSSPGGVVRDEDDKSEPGTEAGAAGQSADGSRAGGGDGGLDDAGLGSGLRHR 117
 Query: 75 GQM-----PE--PSTGFT'ATPP----APDSPQEPLVLRLKFLNDSE---QVAMWP 116
 + PE PS AT P A D+ + +VRLRKFLND+E QV P
 Sbjct: 118 ---ESAGPSTHPPESTPS---ATQPSAEDAASDTHRN-MVLRLKFLNDERTAQVN---P 167
 Query: 117 HDTIGSLKRTQFPGRQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVS---TRVGPP 173
 DTIG +KRT F G+E QRRLIYQGQLL DD+QTL SL+L N VLHCH+S TR
 Sbjct: 168 QDTIGYIKRTYFAGQEHQVRLIYQGQLLQDDSQTLASLNLA DNSVLHCHISQHATR--- 223
 Query: 174 NPPCPPGSEPGPSG-----LEIGSLLLPLLLLLL,LWYCQIQYRPFF--PLTAT 221
 P+G L +GSL++PL +L+L +LWY QIQR FF P TA+
 Sbjct: 224 -----AMPAGARAADQVHVALNVGSJ,MVPLFVLMLSVLWYFQIQYRQFFTAPATAS 274
 Query: 222 LGLAGFTLLSLLAF-MYR 239
 L G T+ S +AF +YR
 Sbjct: 275 --LVGTTTFFSFVAFGVYR 291

[>gi|38091832|ref|XP_126502.2| RIKEN cDNA 2010008E23 [Mus musculus]
 Length = 397
 Score = 158 bits (365), Expect = 4e-37
 Identities = 120/324 (37%), Positives = 161/324 (49%), Gaps = 119/324 (36%)
 Query: 1 TLIEGVGDEVTVLFSVLACL-LVLALAWVSTHTAEGG-----D 37
 TLIEGVG+EV V+ V+A L L LAW+ST+ A+ G D
 Sbjct: 105 TLIEGVGNEVMVVAGVVA-LTLALVLAWLSTYVADSGNNQLLGTIVSAGDTSVLHLGHVD 163
 Query: 38 PL-----PQPSG-----TPTPSQPSMMMTDSMRGEA---PGAETPSLRHKG 75

L P PSG T +DS G+A PGA RG
 Sbjct: 164 QLVNQGTPEPTEHPHPSGGNDDKAEET-----SDSG-GDATGEPGA-----RG 205

Query: 76 QMQPEPS-----TGFATPP-AP---D---SPQEPLV-LRLKFLNDSEQ 111
 +M EPS G ++ P AP D SP L+ +RLKFLND+E+
 Sbjct: 206 EM--EPSLEHLLDIQGLPKRQAGLGSSRPEAPLGLDDGSCLSPSPSLINVRLKFLNDTEE 263

Query: 112 VAM-WPHDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRV 170
 +A+ P DT+G+LK FPG+E Q++LIYQG+LL D +TL SL++ NCV+HCH S
 Sbjct: 264 LAVARPEDTVGTLKSKYFPQESQMKLIYQGRLLQDPARTLSSLNITNNCVIHCHRS--- 320

Query: 171 GPPNPPCPCPGSE-PGPS-----GLEIGSLLLPLLLLLLWYCQIQYRPFF- 216
 PPG+ GPS G+ +GSL++P+ ++LL, ++WY +I YR FF
 Sbjct: 321 -----PPGAAVSGPSASLTPTTEQSSLGVNVGSLMVPVFVVLIGVVWYFRINYRQFFT 373

Query: 217 -PLTATLGLLAGFTLLSLLAF-MY 238
 P AT+ L G T+ S+L F MY
 Sbjct: 374 GP---ATISLVGTVFFSILVFGMY 395

[>gi|16740606|gb|AAH16187.1] RIKEN cDNA 2010008E23 gene [Mus musculus]
 Length = 349

Score = 158 bits (365), Expect = 4e-37
 Identities = 120/324 (37%), Positives = 161/324 (49%), Gaps = 119/324 (36%)

Query: 1 TLIEVGVDVTVLFSVLACL-LVLALAWVSTHTAEGG-----D 37
 TLIEVGVD+EV V+ V+A L L L LAW+S'T+ A+ G D
 Sbjct: 57 TLIEVGVDNEVMVVAGVVA-LTLALVLAWLSTYVADSGNNELLGTIVSAGDTSVLHLGHVD 115

Query: 38 PL-----PQPSG-----TPTPSQPSMMMTDSMRGEA---PGAETPSLRHRG 75
 L P PSG T +DS G+A PGA RG
 Sbjct: 116 QLVNQGTPEPTEHPHPSGGNDDKAEET-----SDSG-GDATGEPGA-----RG 157

Query: 76 QMQPEPS-----TGFATPP-AP---D---SPQEPLV-LRLKFLNDSEQ 111
 +M EPS G ++ P AP D SP L+ +RLKFLND+E+
 Sbjct: 158 EM--EPSLEHLLDIQGLPKRQAGLGSSRPEAPLGLDDGSCLSPSPSLINVRLKFLNDTEE 215

Query: 112 VAM-WPHDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRV 170
 +A+ P DT+G+LK FPG+E Q++LIYQG+LL D +TL SL++ NCV+HCH S
 Sbjct: 216 LAVARPEDTVGTLKSKYFPQESQMKLIYQGRLLQDPARTLSSLNITNNCVIHCHRS--- 272

Query: 171 GPPNPPCPCPGSE-PGPS-----GLEIGSLLLPLLLLLLWYCQIQYRPFF- 216
 PPG+ GPS G+ +GSL++P+ ++LL ++WY +I YR FF
 Sbjct: 273 -----PPGAAVSGPSASLTPTTEQSSLGVNVGSLMVPVFVVLIGVVWYFRINYRQFFT 325

Query: 217 -PLTATLGLLAGFTLLSLLAF-MY 238
 P AT+ L G T+ S+L F MY
 Sbjct: 326 GP---ATISLVGTVFFSILVFGMY 347

[>gi|20988715|gb|AAH29841.1] 2010008E23Rik protein [Mus musculus]
 Length = 309

Score = 158 bits (365), Expect = 4e-37
 Identities = 120/324 (37%), Positives = 161/324 (49%), Gaps = 119/324 (36%)

Query: 1 TLIEGVGDEVTVLFSVLACL-LVLALAWVSTHTAEGG-----D 37
 TLIEGVG+EV V+ V+A L L LAW+ST+ A+ G D
 Sbjct: 17 TLIEGVGNEVMVVAGVVA-LTLALVLAWLSTYVADSGNNQLLGTIVSAGDT'SVLHLGHVD 75

Query: 38 PL-----PQPSG-----TPTPSQPSMMMTDSMRGEA---PGAETPSLRHRG 75
 L P PSG T +DS G+A PGA RG
 Sbjct: 76 QLVNQGTPEPTEHPHPSGGNDDKAEET-----SDSG-GDAT'GEPGA-----RG 117

Query: 76 QMQPEPS-----TGFTATPP-AP----D---SPQEPLV-LRLKFLNDSEQ 111
 +M EPS G ++ P AP D SP L+ +RLKFLND+E+
 Sbjct: 118 EM--EPSLEHLLDIQGLPKRQAGLGSSRPEAPLGLDDGSCLSPSPSLINVRLKFLNDTEE 175

Query: 112 VAM-WPHDTIGSLKRTQFPGRQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRV 170
 +A+ P DT+G+LK FPG+E Q++LIYQG+LL D +TL SL++ NCV+HCH S
 Sbjct: 176 LAVARPEDTVGTLKSKYFPQESQMKLIIYQGRLLQDPARTLSSLNITNNCVIHCRRS--- 232

Query: 171 GPPNPPCPCPGSE-PGPS-----GLEIGSLLLPLLLLLLWYCQIQYRPF- 216
 PPG+ GPS G+ +GSL++P+ ++LL ++WY +I YR FF
 Sbjct: 233 -----PPGAAVSGPSASLTPTEQSSLGVNVGSLMVPVFVLLGVVWYFRINYRQFFT 285

Query: 217 -PLTATLGLLAGFTLLSLLAF-MY 238
 P AT+ L G T+ S+L F MY
 Sbjct: 286 GP--ATISLGVTVFFSILVFGMY 307

[>] >gi|12842172|dbj|BAB25500.1| [■] unnamed protein product [Mus musculus]
 Length = 309

Score = 151 bits (350), Expect = 3e-35
 Identities = 119/324 (36%), Positives = 160/324 (49%), Gaps = 119/324 (36%)

Query: 1 TLIEGVGDEVTVLFSVLACL-LVLALAWVSTHTAEGG-----D 37
 TLIEGVG+EV V+ V+A L L LAW+ST+ A+ G D
 Sbjct: 17 TLIEGVGNEVMVVAGVVA-LTLALVLAWLSTYVADSGNNQLLGTIVSAGDT'SVLHLGHVD 75

Query: 38 PL-----PQPSG-----TPTPSQPSMMMTDSMRGEA---PGAETPSLRHRG 75
 L P PSG T +DS G+A PGA RG
 Sbjct: 76 QLVNQGTPEPTEHPHPSGGNDDKAEET-----SDSG-GDAT'GEPGA-----RG 117

Query: 76 QMQPEPS-----TGFTATPP-AP----D---SPQEPLV-LRLKFLNDSEQ 111
 +M EPS G ++ P AP D SP L+ +RLKFLND+E+
 Sbjct: 118 EM--EPSLEHLLDIQGLPKRQAGLGSSRPEAPLGLDDGSCLSPSPSLINVRLKFLNDTEE 175

Query: 112 VAM-WPHDTIGSLKRTQFPGRQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRV 170
 +A+ P DT+G+LK FPG+E Q++LIYQG+LL D +TL SL++ NCV+HCH S
 Sbjct: 176 LAVARPEDTVGTLKSKYFPQESQMKLIIYQGRLLQDPARTLSSLNITNNCVIHCRRS--- 232

Query: 171 GPPNPPCPCPGSE-PGPS-----GLEIGSLLLPLLLLLLWYCQIQYRPF- 216
 PPG+ GPS G+ +GSL++P+ ++LL ++WY +I YR FF
 Sbjct: 233 -----PPGAAVSGPSASLTPTEQSSLGVNVGSLMVPVFVLLGVVWYFRINYRQFFT 285

Query: 217 -PLTATLGLLAGFTLLSLLAF-MY 238
 P AT+ L G T+ S+L F MY
 Sbjct: 286 GP--ATISLGVTVFFSILVFGMY 307

[>] >gi|28973799|ref|NP_803190.1| [■] hypothetical protein MGC3123 [Homo sapiens]

gi|21739425|emb|CAD38755.1| hypothetical protein [Homo sapiens]
Length = 301

Score = 151 bits (349), Expect = 4e-35
Identities = 120/326 (36%), Positives = 160/326 (49%), Gaps = 121/326 (37%)

Query: 1 TLIEGVGDEVTLFSVLACLLVLAL--AWVSTHTAEGG----- 36
TLIEGVG+EV V+ V+ L+LAL AW+ST+ A+ G
Sbjct: 7 TLIEGVGNEVMVVAGVVV--LILALVLAWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHV 64

Query: 37 -----DP--LPQPS-----GTPTPSQPSMMMTDSMRGEAPGA--- 66
+P LP PS G DS GEA GA
Sbjct: 65 DHLVAGQGNPEPTELPHPSEGNDKEAEEAGEGRG-----DST-GEA-GAGGGV 110

Query: 67 ETPSLRH-----RGQMQPEPSTGFTATPPAP---DS---PQE P-LV-LRLKFLND 108
E PSL H R + G +++P AP DS P P L+ +RLKFLND
Sbjct: 111 E-PSLEHLLDIQGLPKR----QAGAG-SSSPEAPLRSEDSTCLPPSPGLITVRLKFLND 163

Query: 109 SEQVAM-WPHDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPNCVLHCHVS 167
+E++A+ P DT+G+LK FPG+E Q++LIYQG+LL D +TL SL++ NCV+HCH S
Sbjct: 164 TEELAVARPEDTVGALKSKYFPQESQMKLIYQGRLLQDPARTLRSNITDNCVIHCHRS 223

Query: 168 TRVGPPNPPCPCPGSE-PGPS-----GLEIGSLLLPLLLLLLWYCQIQYR 213
PPGS PGPS G+ +GSL++P+ ++LL ++WY +I YR
Sbjct: 224 -----PPGSAVPGPSASLAPSATEPPSLGVNVGSLMVPVFVVLGVVWYFRINYR 273

Query: 214 PFFPLTATLGLAGFTLLSLLAF-MY 238
FF AT+ L G T+ S I F MY
Sbjct: 274 QFFTAPATVSLGVTVFFSFLVFGMY 299

gi|33341676|gb|AAQ15209.1| FP2653 [Homo sapiens]
gi|37182679|gb|AAQ89140.1| ELSD1897 [Homo sapiens]
gi|39645315|gb|AAH63489.1| MGC3123 protein [Homo sapiens]
Length = 301

Score = 151 bits (349), Expect = 4e-35
Identities = 120/326 (36%), Positives = 160/326 (49%), Gaps = 121/326 (37%)

Query: 1 TLIEGVGDEVTLFSVIACLLVLAL--AWVSTHTAEGG----- 36
TLIEGVG+EV V+ V+ L+LAL AW+ST+ A+ G
Sbjct: 7 TLIEGVGNEVMVVAGVVV--LILALVLAWLSTYVADSGSNQLLGAIVSAGDTSVLHLGHV 64

Query: 37 -----DP--LPQPS-----GTPTPSQPSMMMTDSMRGEAPGA--- 66
+P LP PS G DS GEA GA
Sbjct: 65 DHLVAGQGNPEPTELPHPSEGNDKEAEEAGEGRG-----DST-GEA-GAGGGV 110

Query: 67 ETPSLRH-----RCQMQPEPSTGFTATPPAP---DS---PQE P-LV-LRLKFLND 108
E PSL H R + G +++P AP DS P P L+ +RLKFLND
Sbjct: 111 E-PSLEHLLDIQGLPKR----QAGAG-SSSPEAPLRSEDSTCLPPSPGLITVRLKFLND 163

Query: 109 SEQVAM-WPHDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPNCVLHCHVS 167
+E++A+ P DT+G+LK FPG+E Q++LIYQG+LL D +TL SL++ NCV+HCH S
Sbjct: 164 TEELAVARPEDTVGALKSKYFPQESQMKLIYQGRLLQDPARTLRSNITDNCVIHCHRS 223

Query: 168 TRVGPPNPPCPCPGSE-PGPS-----GLEIGSLLLPLLLLLLWYCQIQYR 213
PPGS PGPS G+ +GSL++P+ ++LL ++WY +I YR
Sbjct: 224 -----PPGSAVPGPSASLAPSATEPPSLGVNVGSLMVPVFVVLGVVWYFRINYR 273

Query: 214 PFFPLTATLGLAGFTLLSLLAF-MY 238
 FF AT+ L G T+ S L F MY
 Sbjct: 274 QFFTAPATVSLVGTVFFSFLVFGMY 299

[gi|27689889|ref|XP_221010.1| similar to RIKEN cDNA 2010008E23 gene [Rattus no
 Length = 355

Score = 144 bits (333), Expect = 5e-33
 Identities = 115/323 (35%), Positives = 152/323 (47%), Gaps = 117/323 (36%)

Query: 1 TLIEGVGDEVTLFSV--LACLLVLALAWVSTHTAEGG----- 36
 TLIEGVG+EV V+ V L L L LAW+ST+ A+
 Sbjct: 63 TLIEGVGNEVMVVAGVVVLT--LALVLAWLSTYVADSSNSQLLGTIVSAGDTSVLHLGIIV 120

Query: 37 DPL-----PQPSG-----TPTPSQPSMMMTDS---MRGEAPGAETPSLRHR 74
 D L P PSG T +DS GE PGA R
 Sbjct: 121 DQLVNQGTPEIPTEHPHPSGGSDDKAEET-----SDSGGDTTGE-PGA-----R 162

Query: 75 GQMQEPEPS-----TGFTATPPAP----DS---PQEPLV-LRLKFLNDSE 110
 G M EPS G ++ P DS P L+ +RLKFLND+E
 Sbjct: 163 GDM--EPSLEHLLDIQGLPKRQAGLESSRPEASLGLDDSTCLSPSPSLINVRKFLNDTE 220

Query: 111 QVAM-WPHDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTR 169
 ++A+ P DT+G+LK FPG+E Q++LIYQG+LL D +TL SL++ NCV+HCH S
 Sbjct: 221 ELAVARPEDETVGTLKSKYFPQESQMKLIYQGRLLQDPARTLSSINITNNCVIHCHR-- 278

Query: 170 VGPPNPPCPCPGSE-PGPS-----GLEIGSLLLPLLLLLLWYCQIQYRPFF 216
 PPG+ GPS G+ +GSL++P+ ++LL ++WY +I YR FF
 Sbjct: 279 -----PPGAAVSGPSTSITPTTEQSSLGVNGSLMVPVFVLLGVVWYFRINYRQFF 330

Qucry: 217 PLTATLGLAGFTLLSLLAF-MY 238
 AT+ L G T+ S L F MY
 Sbjct: 331 TAPATVSLVGTVFFSFLVFGMY 353

[gi|22204247|emb|CAD43429.1| SI:dZ180G5.5 (novel ubiquitin) [Danio rerio]
 Length = 291

Score = 108 bits (249), Expect = 2e-22
 Identities = 68/159 (42%), Positives = 89/159 (55%), Gaps = 33/159 (20%)

Query: 102 RLKFINDSEQVA-MWPHDTIGSLKRTQFPGREQQVRLIYQGQLLGDDTQ-TLGSILHLPPN 159
 RLKFLND+E++A + P DTIG LK F GRE Q++LIYQGQLL D Q +L SL++ N
 Sbjct: 140 RLKFLNDTEEEIAVLRPQDTIGLLKSKYFSGREHQIKLIYQGQLL-QDPQRSLLSLNITHN 198

Query: 160 CVLHCHVS---TRVGPPNPPCPCPGSEPGP-----SG-----LEIGSLLLPLL 199
 VLHCH+S R +E GP SG L G L++P+ +
 Sbjct: 199 SVLHCHISQAQAQR-----EAAEDGPRASRVSILSGGLRSAGVALSTGGLVIPVVF 249

Query: 200 LLLLLLWYCQIQYRPFFPLTATLGLAGFTLLSLLAF-M 237
 +LL ++WY +I YR F AT+ L G T+ S L F M
 Sbjct: 250 VLLAVVWYFRINYRQLFTAPATISLVGTVFFSFLIFGM 288